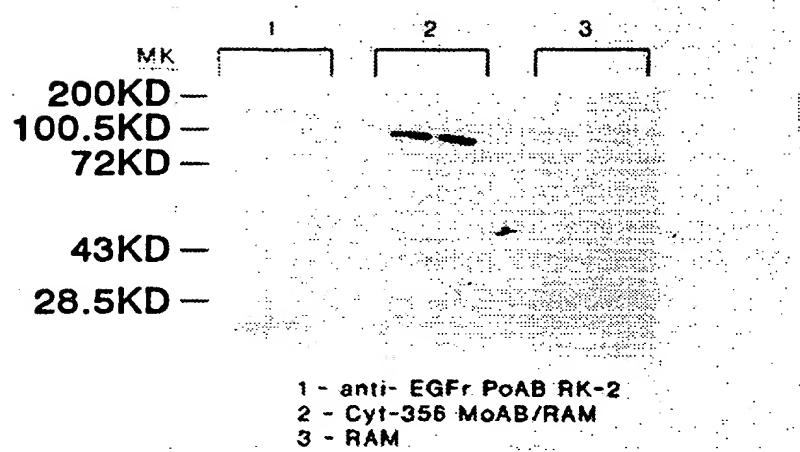


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FIGURE 1



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FIGURE 2A

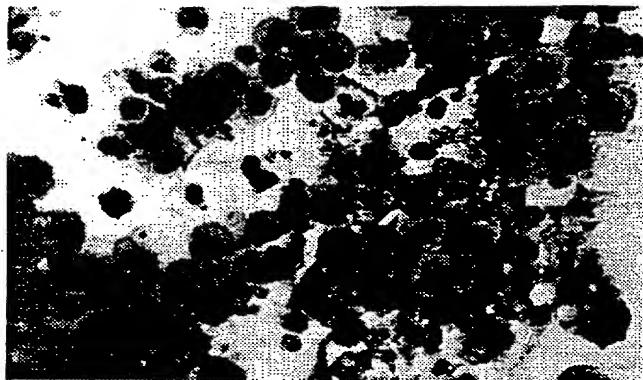


FIGURE 2B

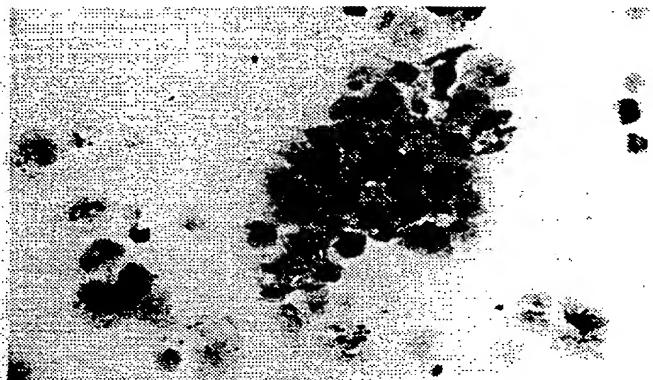


FIGURE 2C

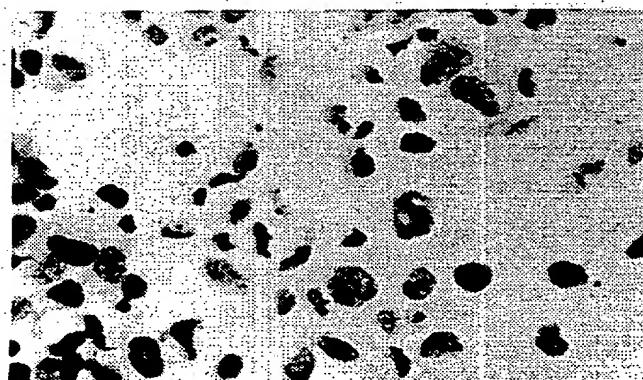
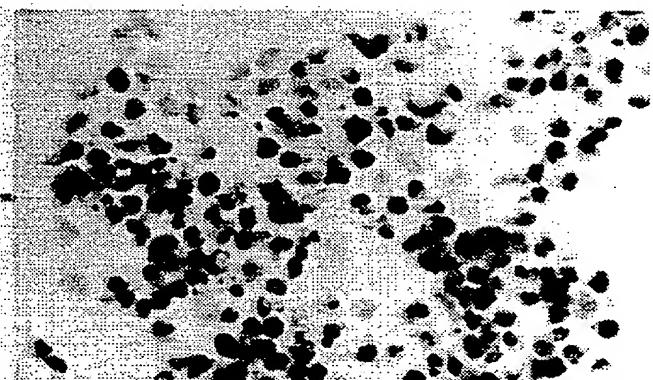
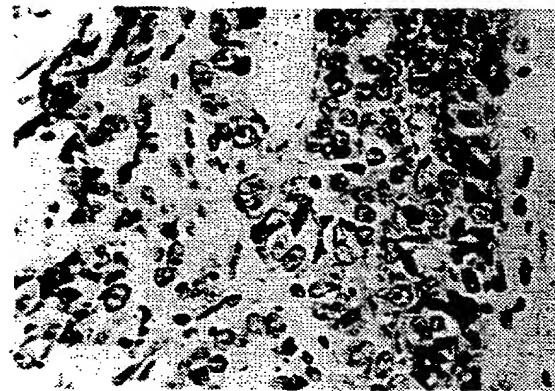
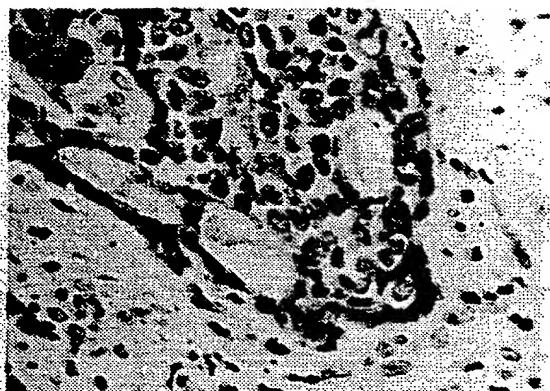
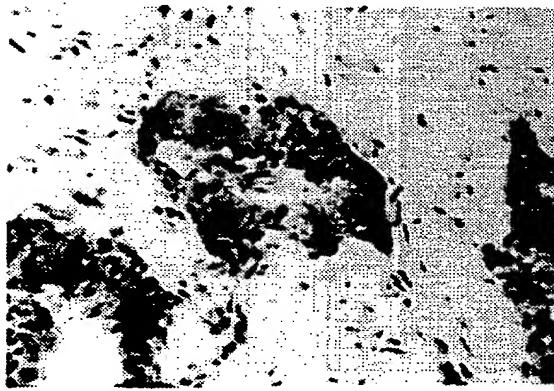
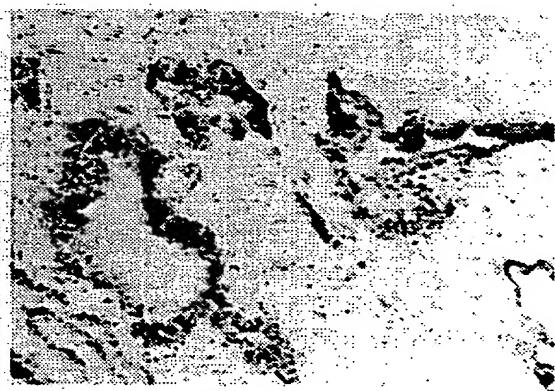


FIGURE 2D



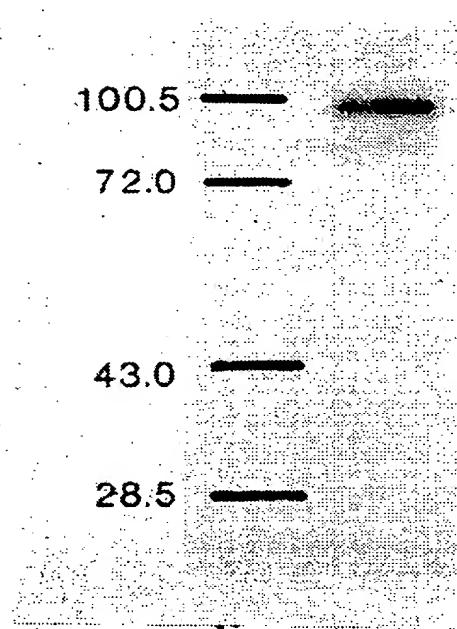
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FIGURE 3A**FIGURE 3B****FIGURE 3C****FIGURE 3D**

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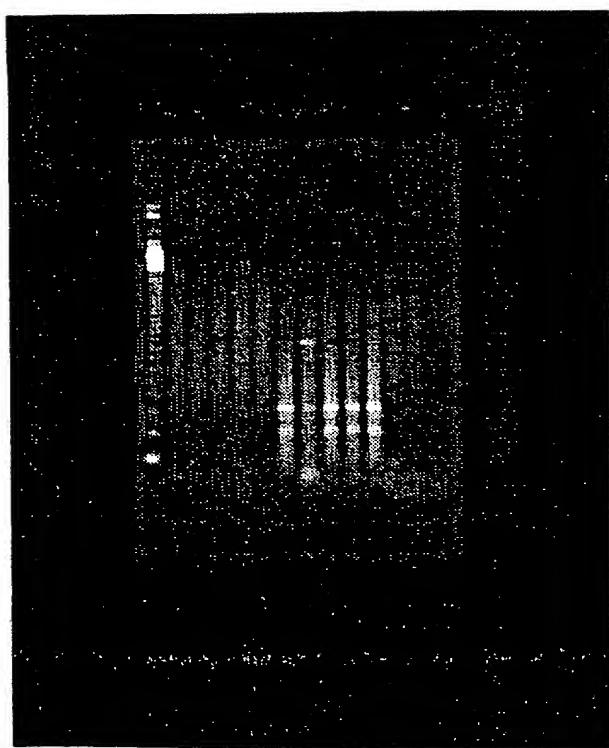
FIGURE 4



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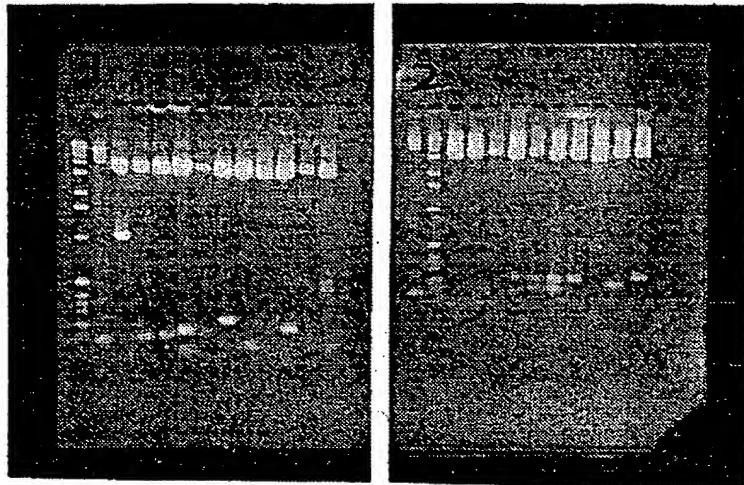
FIGURE 5



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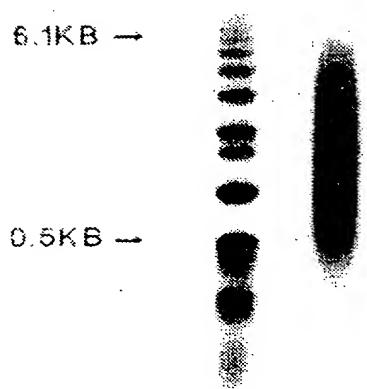
FIGURE 6A FIGURE 6B



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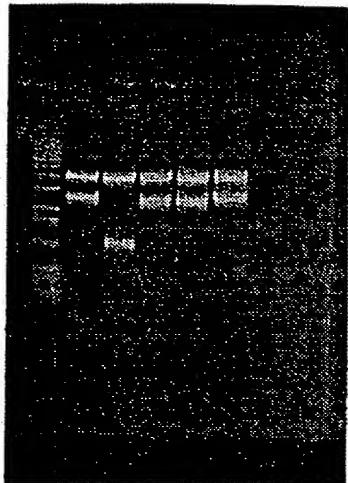
FIGURE 7



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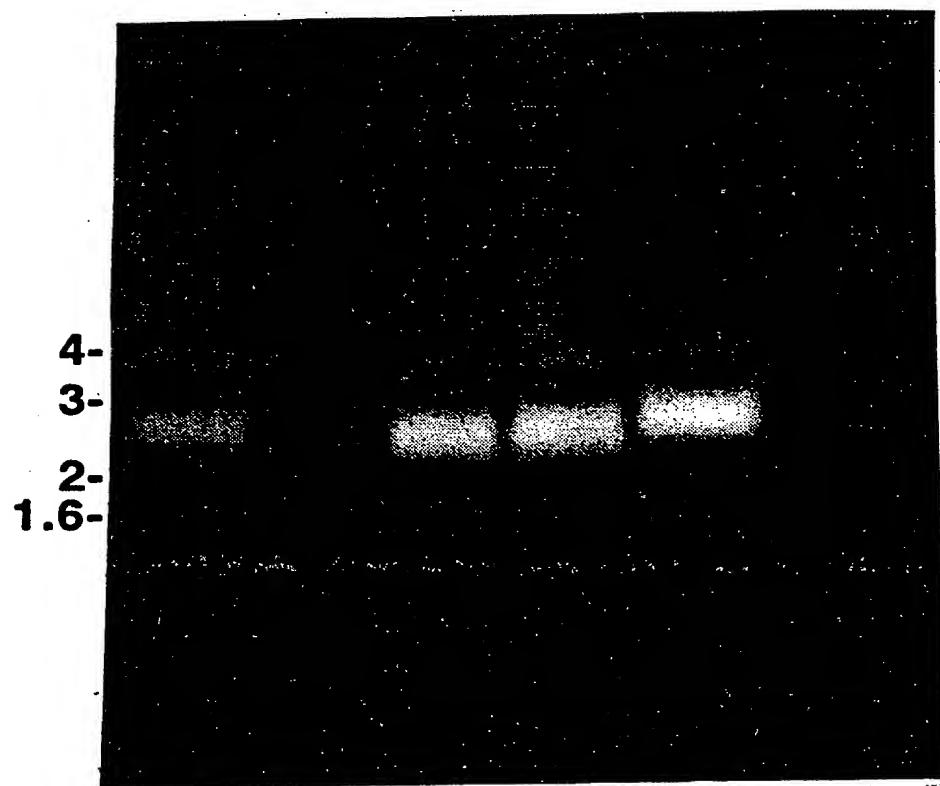
FIGURE 8



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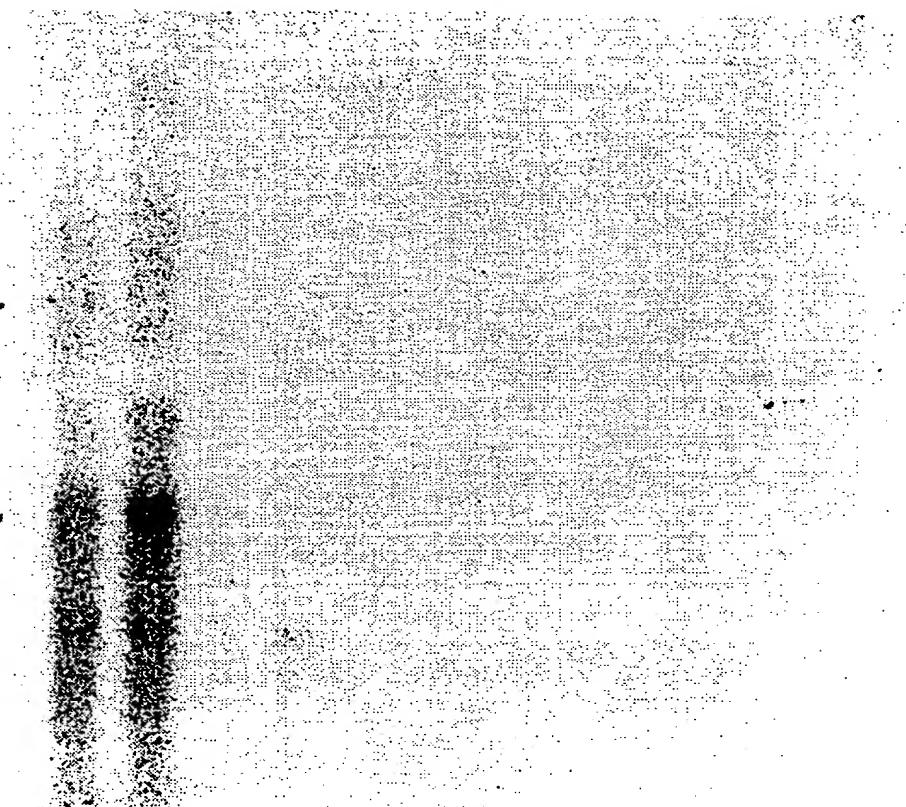
FIGURE 9



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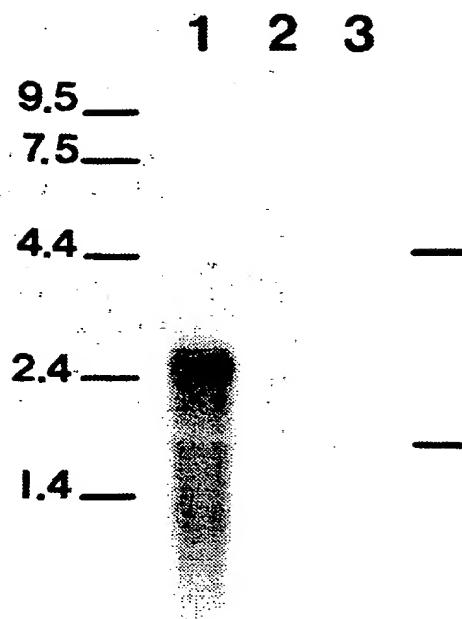
FIGURE 10



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FIGURE 11



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FIGURE 12A

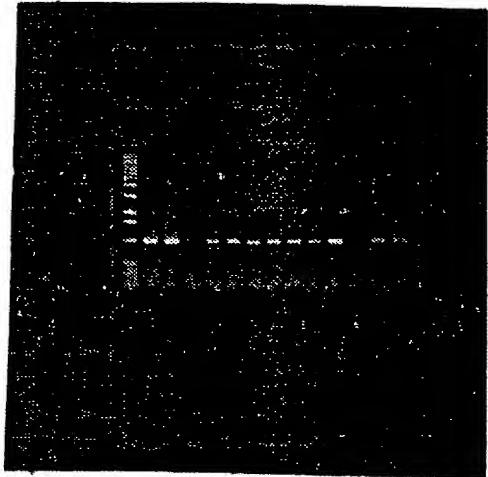
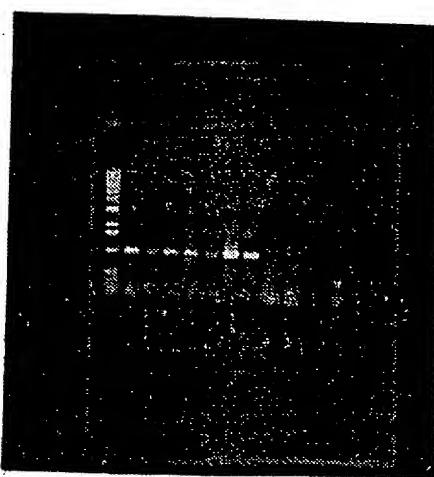


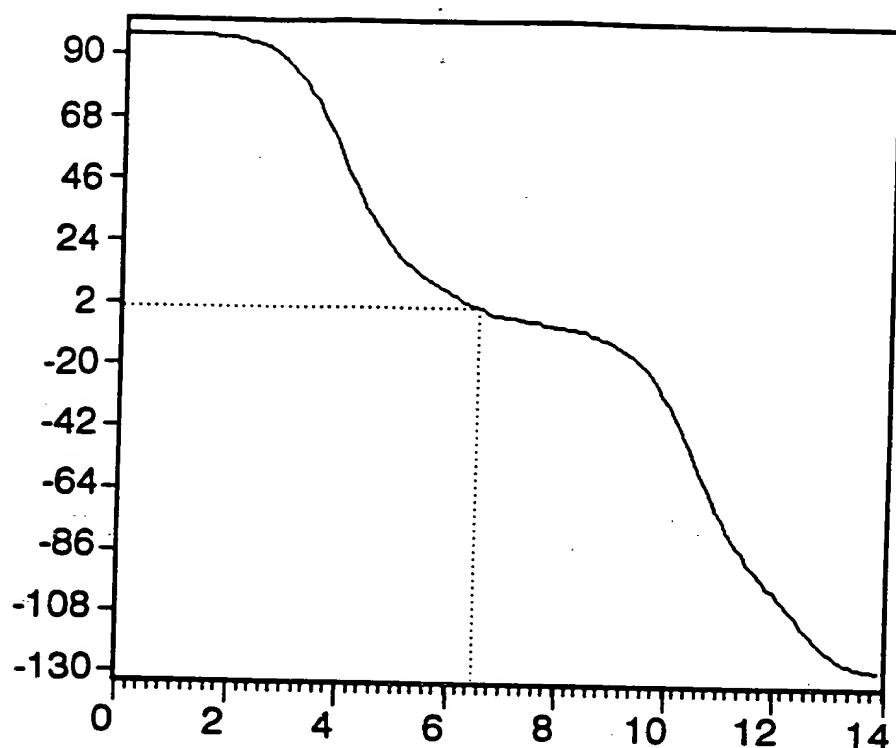
FIGURE 12B



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FIGURE 13



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FIGURE 14-1

Done on sequence PMSANTIGEN.
 Total number of residues is: 750.
 Analysis done on the complete sequence.

In Helical (H) conformation [DC = -75 CNAT] : 264 AA => 35.2%
 In Extended (E) conformation [DC = -88 CNAT] : 309 AA => 41.2%
 In Turn (T) conformation [DC = 0 CNAT] : 76 AA => 10.1%
 In Coil (C) conformation [DC = 0 CNAT] : 101 AA => 13.4%

Sequence shown with conformation codes.
 =====

Consecutive stretch of 5 or more residues in a given conformation are overlined.

1 H H H H H H H H H H H H H H E E E T T E E E E E E E E E E E
 31 E E E E E H H H H H H C C C C T H H H H H H H H H H H H H H H
 61 H H H H H H H H H H H H E E E T T E E E C C C C C C C C C C

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FIGURE 14-2

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FIGURE 14-3

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FIGURE 14-4

Semi-graphical output.

ssymbols used in the semi-graphical representation:

Helical conformation: x
Turn conformation: >
Extended conformation: -
Coil conformation: *

10 MNLLHETDSAVATARRPRWLCAAGALVLAGGFFLLGFLFGWFIKSNEAT
 20 XXXXXXXXXX-->>
 30 XXXXXXXXXX-->>
 40 XXXXXXXXXX-->>
 50
 60 NITPKHNMKAFLDELKAENIKKFLYNFQTQIPHILAGTEQMNFLQAKQIQSOW
 70
 80
 90
 100

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FIGURE 14-5

XXXXXXXXXX-->----*-*-*-*XXXXXXX-X*--
XXXXXXXXXX-->----*-*-*-*XXXXXXX-X*--

110 120 130 140 150
| | | |
KEFGLDSVELAHYDVLLSYPNKTHPNYISIINEDGNEIFNTSLFEP PPPG

->>* *XXXXXXX---->>* *---->* *---->>* *---->>
->>* *XXXXXXX---->>* *---->* *---->>* *---->>

160 170 180 190 200
| | | |
YENVSDIVPPFSAFSPQGMPEGDLVYVNYARTEDFFKLERDMKINCSGKI

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FIGURE 14-6

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FIGURE 14-7

-----* * *>---->* * *>* * XXX-----XX
 -----* * *>---->* * *>* * XXX-----XX
 -----* * *>---->* * *>* * XXX-----XX

410 420 430 440 450
 SFGTLLKKEGWRPRRTILFASWDAEEFGLLGSTEWAEEENSRLLQERGVAYI

-----* * *>>>* * *>---->* XXXXXXXX* * *# XXXXXXXX-----
 -----* * *>>>* * *>---->* XXXXXXXX* * *# XXXXXXXX-----
 -----* * *>>>* * *>---->* XXXXXXXX* * *# XXXXXXXX-----

460 470 480 490 500
 NADSSIEGNYTLRVVDCTPLMYSLVHNLTKELKSPDEGFEGKSLYESWTK
 -----* * --->>---->* XXXXXXXX* * XXXXXXXX>>>
 -----* * --->>---->* XXXXXXXX* * XXXXXXXX>>>

510 520 530 540 550
 SPSPEFSGMPRISKLGSNDFFEVFFQRLGIASGRARYTKNWETNKFSGYP
 -----* * *>---->* * *#----XXX>* * *#---->>>>>>>>
 -----* * *>---->* * *#----XXX>* * *#---->>>>>>>>

560 570 580 590 600
 -----|-----|-----|-----|

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FIGURE 14-8

LYHSVYETYELVEKFYDPMFKYHILTVAQVRGGMVFELANSIVILPFDCCRDY

-----X*****-----X----->XXX
-----X*****-----X----->XXX
-----X*****-----X----->XXX

610 620 630 640 650
| | | |
AVVLRKYADKIVSISMKHPQEMKTYSVSFDLSLFSAVKNFTEIASKFSERL

-----X**-----X----->XXXXXX
-----X**-----X----->XXXXXX
-----X----->XXXXXX

660 670 680 690 700
| | | |
QDFDKSMPIVLRRMNDQLMCCLERAFAIDPLGLPDRPFYRHVIYAPSSHINKY

XX>>*-----XXXXXX-->>* * * >----->* * * * >
XX>>*-----XXXXXX-->>* * * >----->* * * * >

710 720 730 740 750
| | | |
AGESFPGIYDALFDIESKVDPSKAWGEVKRQIYVAAFTVQAAAETLSEVA

----->--XXXXXX* * * XXXXXXXX----->XXXXXX
----->--XXXXXX* * * XXXXXXXX----->XXXXXX

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FIGURE 15A

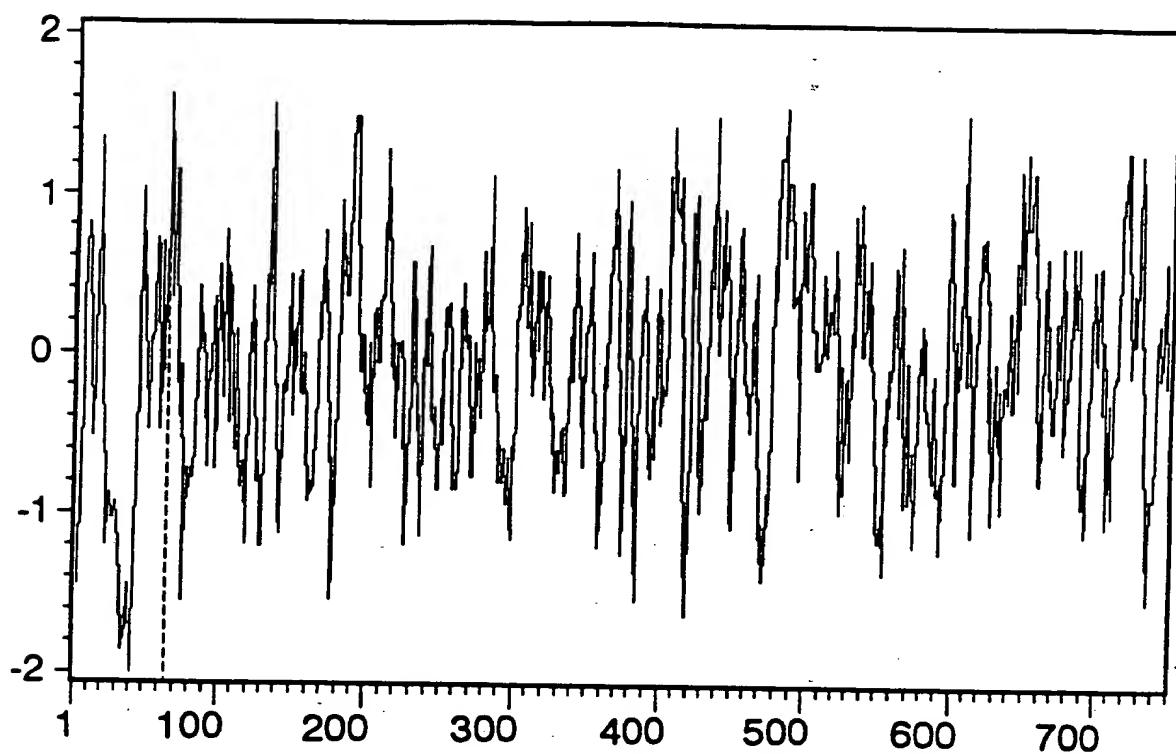


FIGURE 15B

 * PREDICTION OF ANTIGENIC DETERMINANTS *

Done on sequence PMSANTIGEN.
 Total number of residues is: 750.
 Analysis done on the complete sequence.

The method used is that of Hopp and Woods.
 The averaging group length is: 6 amino acids.
 -> This is the value recommended by the authors <-

The three highest points of hydrophilicity are:

(1) Ah= 1.62 : From 63 to 68 : Asp-Glu-Leu-Lys-Ala-Glu
 (2) Ah= 1.57 : From 132 to 137 : Asn-Glu-Asp-Gly-Asn-Glu
 (3) Ah= 1.55 : From 482 to 487 : Lys-Ser-Pro-Asp-Glu-Gly

Ah stands for: Average hydrophilicity.

Note that, on a group of control proteins, only the highest point was in 100% of the cases assigned to a known antigenic group. The second and third point gave a proportion of 33% of incorrect predictions.

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The best scores are:
 CHKTFER G. gallus mRNA for transferrin receptor 203 120 321
 RATTRFR Rat transferrin receptor mRNA, 3' end. 164 164 311
 HUMTFR Human transferrin receptor mRNA, complete cd 145 145 266

FIGURE 16-1

initn init1 opt
 CHKTFER G. gallus mRNA for transferrin receptor 203 120 321
 RATTRFR Rat transferrin receptor mRNA, 3' end. 164 164 311
 HUMTFR Human transferrin receptor mRNA, complete cd 145 145 266

CHKTFER G.gallus mRNA for transferrin receptor 203 120 321
 51.9% identity in 717 nt overlap

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1020	1030	1040	1050	1060	1070
pmssgen	TGTCCAGCGTGGAAATATCCTAAATCTGAATG	GTGCAGGAGACCCCTCTCACACCAGGTTA	:::	:::	:::
CHKTFE	TACACTTATCCCATCGGACATGCCAACCTTG	GAACCTTGAGACCCCTTACACCCCCAGGCTT	:::	:::	:::
	990	1000	1010	1020	1030
					1040
1080	1090	1100	1110	1120	1130
pmssgen	CCCAGGAAATGAATATGCTTATAGGCCGTTAGG	GAATTGCAGAGGCTGGTCTTCCAACTAT	GGCT	GGCT	GGCT
CHKTFE	CCCTTCGTTCAACCACCCA---GTTTCCACCA	GTTGAATCTTCAGGACTACCCACAT	:::	:::	:::
	1050	1060	1070	1080	1090
					1100
1140	1150	1160	1170	1180	1190
pmssgen	TCCTGTTCAATTGGATACTATG	GCACAGAAAGCTCCCTAGAAAAATGGGTGGCTC	:::	:::	:::
CHKTFE	GACCATTCTCTAGCAGTGCAGGCCAGG	GCTTCAAGCAAAATGGATGGAGA	:::	:::	:::
	1110	1120	1130	1140	1150
					1160

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FIGURE 16-2

1200	1210	1220	1230	1240	1250
pmsgen	AGCACCAAGATAGCAGGCTGGAGAGGAAGTCTCAAAGTCCCCTACAATGTTGGACCTGG				
:	:	:	:	:	:
CHKTFE	CACATGCTCTGA-AG--GTTGGAAAGGTGGCATCCA---TTCCCTGTAAGGT--GAC--AA				
1170	1180	1190	1200	1210	

1260	1270	1280	1290	1300	1310
pmsgen	CTTTACTGGAAACTTTCTACACAAAAAAGTCAAGATGGCACATCCACTCTACCAATGAACT				
:	:	:	:	:	:
CHKTFE	CAAAGCAGGAGA---GCCAGA-TAATGGTGAAACTAGATGTGAAGAACATTCCATGAAAGA				
1220	1230	1240	1250	1260	

1320	1330	1340	1350	1360	1370
pmsgen	GACAAGAATTACAATGTTAGGTACTCTCAGAGGAGGCTGGAAACCAAGACAGATATGT				
:	:	:	:	:	:
CHKTFE	CAGGAAGAATTCTGAACATCTTCGGTGCATTCAGGGATTGAAAGAACCTGATCCGGTATGT				
1270	1280	1290	1300	1310	1320

1380	1390	1400	1410	1420	1430
pmsgen	CATTCTGGGAGGTCAACCGGACTCATGGGTATTGACCCCTCAGAGTGGAGC				
:	:	:	:	:	:
CHKTFE	TGTGATTGGAGGCCAGAGAGACTCCCTGGGGCCAGGAGTGGCTAAAGCTGGCACTGGAAC				
1330	1340	1350	1360	1370	1380

FIGURE 16-3

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pmsgen	AGCTGTGTTCATGAAATTGTGAG	1440	1450	1460	1470	1480	1490
CHKTFE	TGCTATATTGTTGAACTTGCCGTTGATCTCAGACATAGTGA	1390	1400	1410	1420	1430	1440
pmsgen	ACCTAGAAGAACAAATTGTTGCAAGCTGGATGCCAGAAGAATT	1500	1510	1520	1530	1540	1550
CHKTFE	ACCGAGGCCAAGGCATCATCTTGCTAGCTGGAGTGCAGGAGACTACGGAGCTTGCTGGGTGC	1450	1460	1470	1480	1490	1500
pmsgen	TACTGACTGGCAGGGAGAATTCAAGAACCTCCTCAAGAGCGCTGGCTTATATTAA	1560	1570	1580	1590	1600	1610
CHKTFE	TACTGAATTGGCTGGACGGGTACTCTGCCATGCTGCCATTACATCA-	1510	1520	1530	1540	1550	1560
pmsgen	TGC-TGACTCATCTATAGAAGGAAACTA-CACTCTGAGAGTTGATTGATCACCCGCTGATG	1620	1630	1640	1650	1660	1670
CHKTFE	-GCTTGGATGCTCCAGTCAGGAGCAAGCCATGCTCAAGAGATTCTGCCAGCCCCCTGCTG	1570	1580	1590	1600	1610	1620

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FIGURE 16-4

1680 1690 1700 1710 1720 1730
pmsgen TACAGCTTGGTACACAAACCTAACAAAAGAGCTGAAAGCCCTGATGAAGGCTTGTGAAGGC
::: ::: ::: ::: ::: ::: :::
CHKTFE TATATGCTGGGGAGTATTATGAAGGGGGTGAAGGAATCCAGCAGCAGTCTCAGAGGC
1630 1640 1650 1660 1670 1680

1740 1750 1760 1770 1780 1790
pmsgen AAATCTTTATGAAAGTTGGACTAAAAAAGTCCTTCCCCAGACTTCAGTGGCATGCC
::: ::: ::: ::: ::: :::
CHKTFE ----CTCTATAACAGACTTGGCCAGACTGGGTAAAAGCAGTTGTTCCCTTGGCCTGGGA
1690 1700 1710 1720 1730

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FIGURE 16-5

RATTRFR Rat transferrin receptor mRNA, 3' end.
55.5% identity in 560 nt overlap

1210 1220 1230 1240 1250
pmsgen CCACAGATAGCAGGCTGGAGAGGAAGTCTCAAAGTGCCTACAAATGTTGGACCTGGCTT-
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RATTRF TGCAGAAAAGCTATTCAAACATGGAAGGAAACTGTCCTAGTTGGAATAATAGATTC
610 620 630 640 650 660
1260 1270 1280 1290 1300 1310
pmsgen -TACTGGAAACTTTCTACACAAAAGTCAAGATGCACATC-CACTCT-ACCAATG----
RATTRF CTCATGTAAGCTGGAACTTTCACAGAATCAAATGTGAAGGCTCACTGTGAACAAATGTACT
670 680 690 700 710 720

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FIGURE 16-6

1380	1390	1400	1410	1420	1430
pmsgen	ATATGTCATTCTGGAGGTCACCGGGACTCATGGGTATTGACCCCTCAGAG				
790	800	810	820	830	840
RATTRF	CTACATTGTAGTAGGAGGCCAGAGAGACGGCTTGGGGCCCTGGT-GTTGCGAAGTCCAGTG				

1440	1450	1460	1470	1480
pmsgen	T-GGAGCAGCTGTTCATGAAATTGAGGCTTGGAAACA-CTGA---AAAAGGAA			
850	860	870	880	890
				900
				RATTRF TGGAACAGGTCTT-CTGTTGAAACTTGGCCAAAGTATTCTCAGATATGATTCAAAGAT

pmsgen	1490	1500	1510	1520	1530	1540
	GGGTGGGACCTAGAACAAATTGTTGCAAGGCTGGGATGCAGAAGAATTGGCTCTT					
	:::	X:::	:::	:::	:::	:::
RATTRF	910	920	930	940	950	960
	GGATTAGACCCAGGAGTATTATCTTGGCTGCCAGGACTGCAGGAGACTATGGAGCT					

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FIGURE 16-7

1550	1560	1570	1580	1590	1600
pmsgen	CTTGGTTCTACTGAGTGGCAGAGGAGAA	---TTCAAGACTCCTTCAAGAGCGTGGCGTG			
	::: :: : : : : :: :: :: ::	X :: :: :: :: :: :: :: ::			
RATTRF	GTTGGTCCGACTGAGTGGCTGGAGGGTACCTT	TCATCTAAAG---GCTTTC			
	970	980	990	1000	1020
1610	1620	1630	1640	1650	1660
pmsgen	GCTTATTAAATGCTGACTCATCTATAGAAGGAAACTA	-CACTCTGAGAGTTGATTTGTC			
	::: :: : : :: :: :: ::	:: :: :: :: :: :: :: ::			
RATTRF	ACTTACATTAAAT-CTGGATAAAGTCGTTCCCTGGGTACTAGCAACT	CAAGGTTCTGCCAG			
	1030	1040	1050	1060	1070
1670	1680	1690	1700	1710	1720
pmsgen	ACCGCTGATGTACAGCTTGGTACACAACTTAACAAAAGAGCTGAAAGC	-CCTGATGAAG			
	:: :: : : :: :: ::	:: :: :: :: :: :: ::			
RATTRF	CCCCCTATTATAACACTTATGGGAAAGATAATGCAGGA	--CGTAAAGCATCCGA	---		
	1090	1100	1110	1120	1130

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FIGURE 16-8

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FIGURE 16-9

HUMTFR Human transferrin receptor mRNA, complete cd 145 145 266
 54.3% identity in 464 nt overlap

1230 1240 1250 1260 1270
 pmsgen AGGAAGTCTCAAAGTGCCTTACAAATGTTGGACCTGGCTTAC-TGGAAACTTTCTACAC
 :
 HUMTFR TATGGAAGGAGACTGTCCCTCTGACTGGAAAACAGACTCTACATGTTAGGATGGTAAACCTC
 1140 1150 1160 1170 1180 1190

1280 1290 1300 1310 1320 1330
 pmsgen AAAAAGTCAGATGCCACATC-CAACTCT-ACCAATG-----AAGTGACAAGAAATTACAA
 :
 HUMTFR AGAAAGCAAGAATGTGAAGGCTCAACTGTGAGCAAATGTGCTGAAAGAGATAAAATTCTTAA
 1200 1210 1220 1230 1240 1250

1340 1350 1360 1370 1380 1390
 pmsgen TGTGATAGGTACTCTCAGGGAGCCAGTGGAAACCAAGACAGATATGTCATTCTGGGAGGGTCA
 :
 HUMTFR CATCTTGGAGTTATTAAAGGCTTTGTAGAACCAAGATCACTATGTTGTTAGTGTGGGGCCA
 1260 1270 1280 1290 1300 1310

1400 1410 1420 1430 1440 1450
 pmsgen CCGGGACTCATGGGTGTTGGTATTGACCCCTCAGAGT-GGAGCAGCTGTTCTCATG
 :
 HUMTFR GAGAGATGCCATGGGGCCCTGGAGGCTGCAAATC-CGGTGTAGGCACAGCTCCTATTGA
 1320 1330 1340 1350 1360 1370

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FIGURE 16-10

1460 1470 1480 1490 1500
 pmsgen AAATTG---TGAGGAGCTTGGAACACTGAAAAAGGAAGGGCTGGAGACCTAGAAGAACAA
 ::::: ::::: ::::: ::::: :::::
 HUMTFR AACCTGCCAGATGGTCTCAGATATGGTCTAAAGATGGCTTCAGCCCAGCAGAACCA
 1380 1390 1400 1410 1420 1430

1510 1520 1530 1540 1550 1560
 pmsgen TTTTGTGTTGCAAGGCTGGATGCAGAAGAATTGGTCTTGGTTCTACTGAGTGGCCAG
 ::::: ::::: ::::: ::::: ::::: :::::
 HUMTFR TTATCTTGGCCAGTTGGAGACTTGGATCGGTTGGACTTGGCTAATGGCTAG
 1440 1450 1460 1470 1480 1490

1570 1580 1590 1600 1610 1620
 pmsgen A-GGAGAAATTCAAGACTCCTCAAGAGCGTGGCTGGCTTATTAATGGCTGACTCATCT
 ::::: ::::: ::::: ::::: ::::: :::::
 HUMTFR AGGGATACCTTTCGTC-CCTGCATTAAAGGCTTCACTTATTAATCTGGATAAAGCG
 1500 1510 1520 1530 1540 1550

1630 1640 1650 1660 1670 1680
 pmsgen ATAGAAGGAAACTACACTCTGAGAGTGTGATTGTACACCGCTGATGTACA-GCTTGCT-AC
 ::::: ::::: ::::: ::::: ::::: :::::
 HUMTFR GTTCTTGGTACCAAGCAACTCAAGGTCTGGCCAGCCCACGTGTATACGCTTATTGAG
 1560 1570 1580 1590 1600 1610

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FIGURE 16-11

1690 1700 1710 1720 1730 1740
pmsgen ACAACCTAACAAAGAGCTGAAAAGCCCTGATGAAAGGCTTTGAAAGGCCAAATCCTCTTATG
: : : : : :
1620 1630 1640 1650 1660 1670
HUMTFR AAAACAAATGCTGAAGCATCCGGTTACTGGCAATTCTATCAGGACAGCAAC

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FIGURE 17A



FIGURE 17B

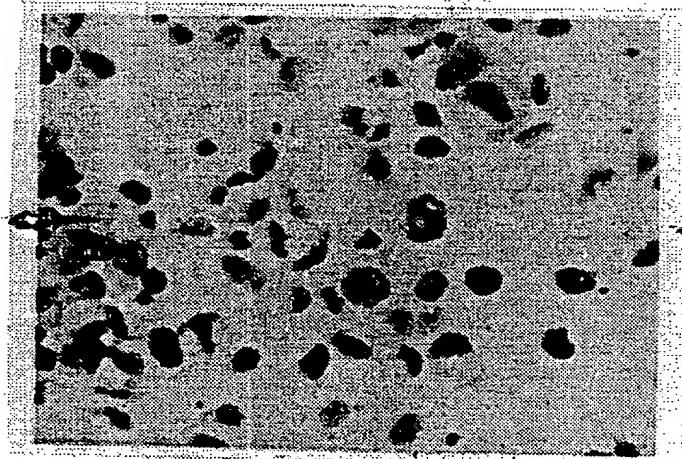
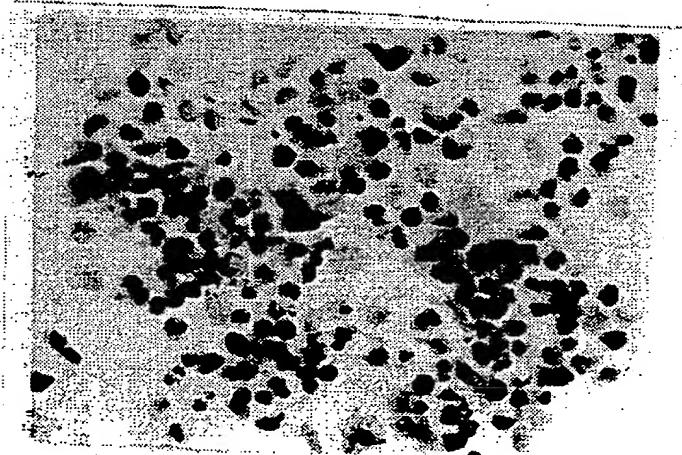


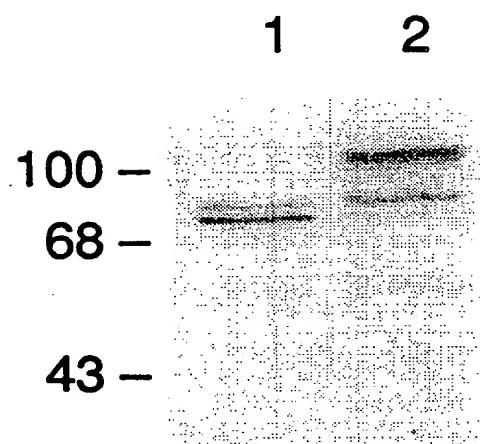
FIGURE 17C



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FIGURE 18

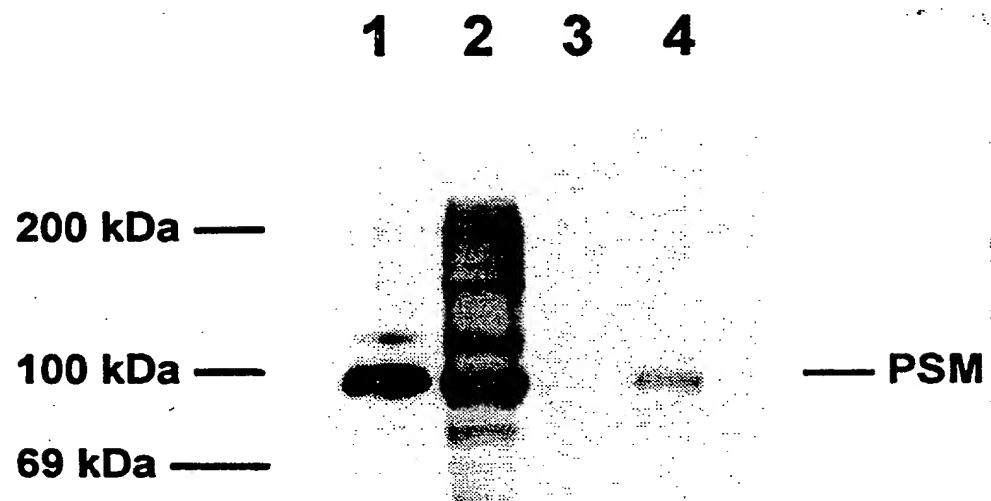


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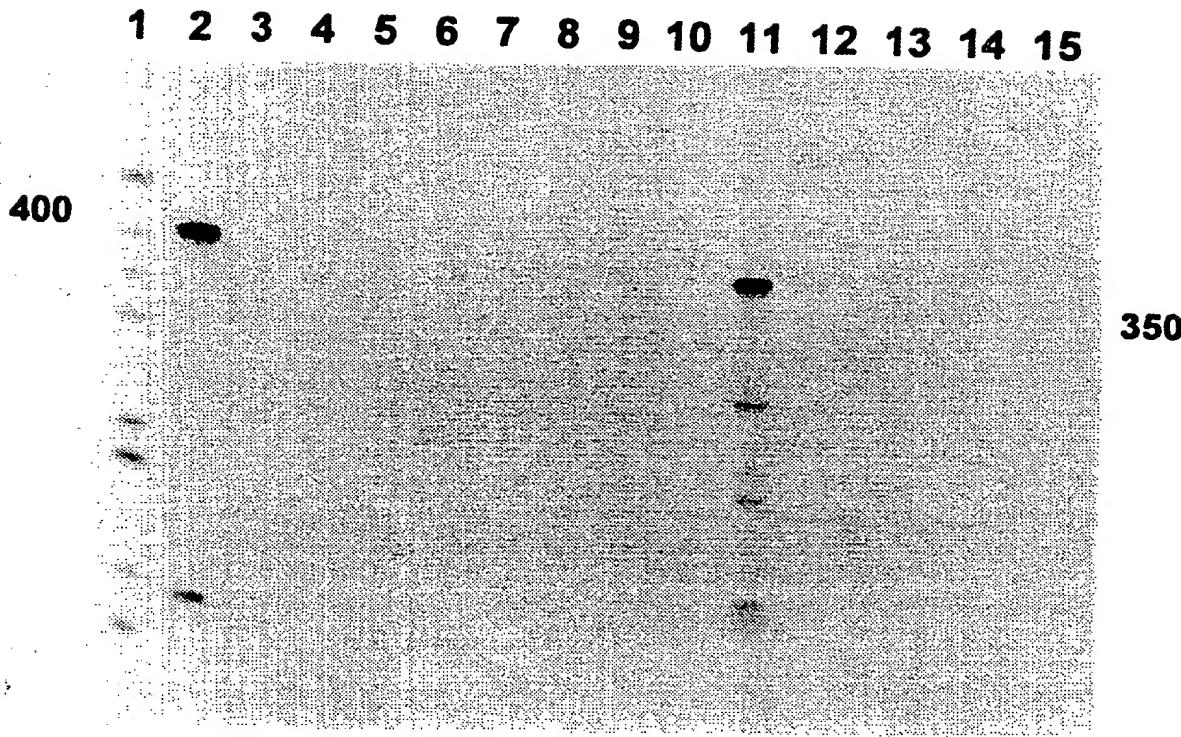
FIGURE 19



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FIGURE 20



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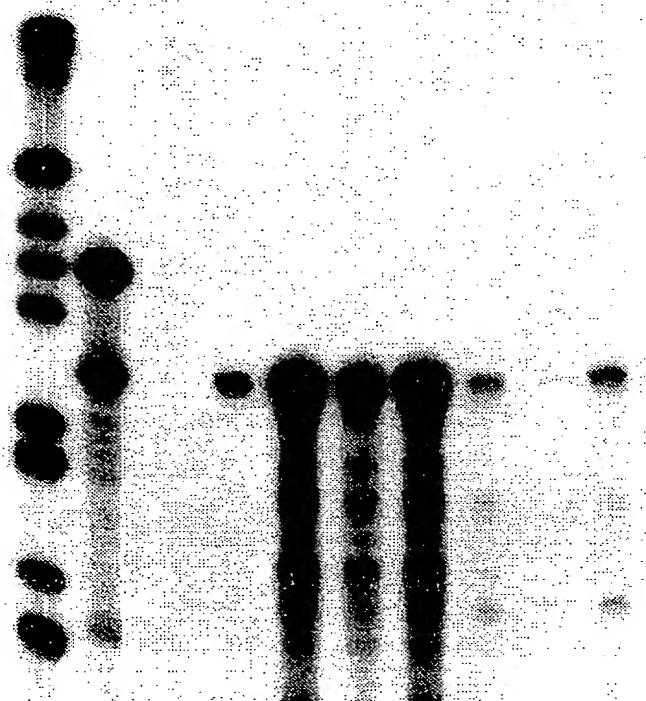
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FIGURE 21

1 2 3 4 5 6 7 8 9 10

298 bp

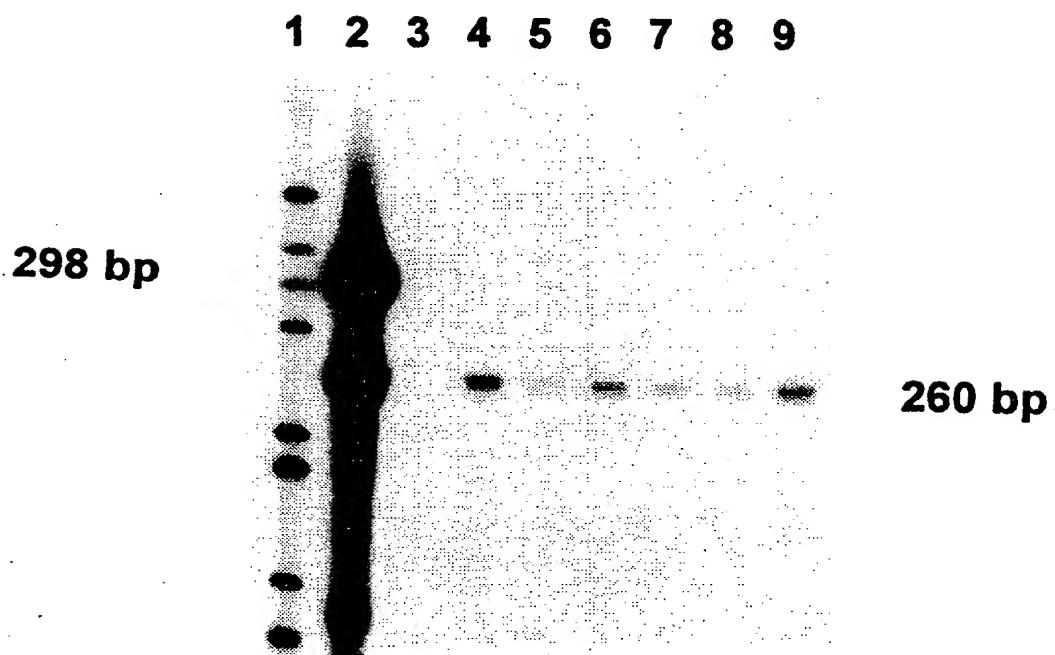
260 bp



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FIGURE 22



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FIGURE 23

CELL LINE/TYPE	11p11.2-13 REGION	METASTATIC	PSM RNA DETECTED	PSM DNA DETECTED
LNCap			++	ND
HUMAN PROSTATE			++	ND
A9 (FIBROSARCOMA)	NO	NO	-	-
A9(11) (A9+HUM. 11)	YES	NO	-	REPEAT
AT6.1 (RAT PROSTATE)	NO	YES	-	-
AT6.1-11-c11	YES	NO	+	++
AT6.1-11-c12	NO	YES	-	-
R1564 (RAT MAMMARY)	NO	YES	-	-
R1564-11-c14	YES	YES	-	+
R1564-11-c15	YES	YES	-	REPEAT
R1564-11-c16	YES	YES	-	ND
R1564-11-c12	YES	YES	ND	+

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FIGURE 24A

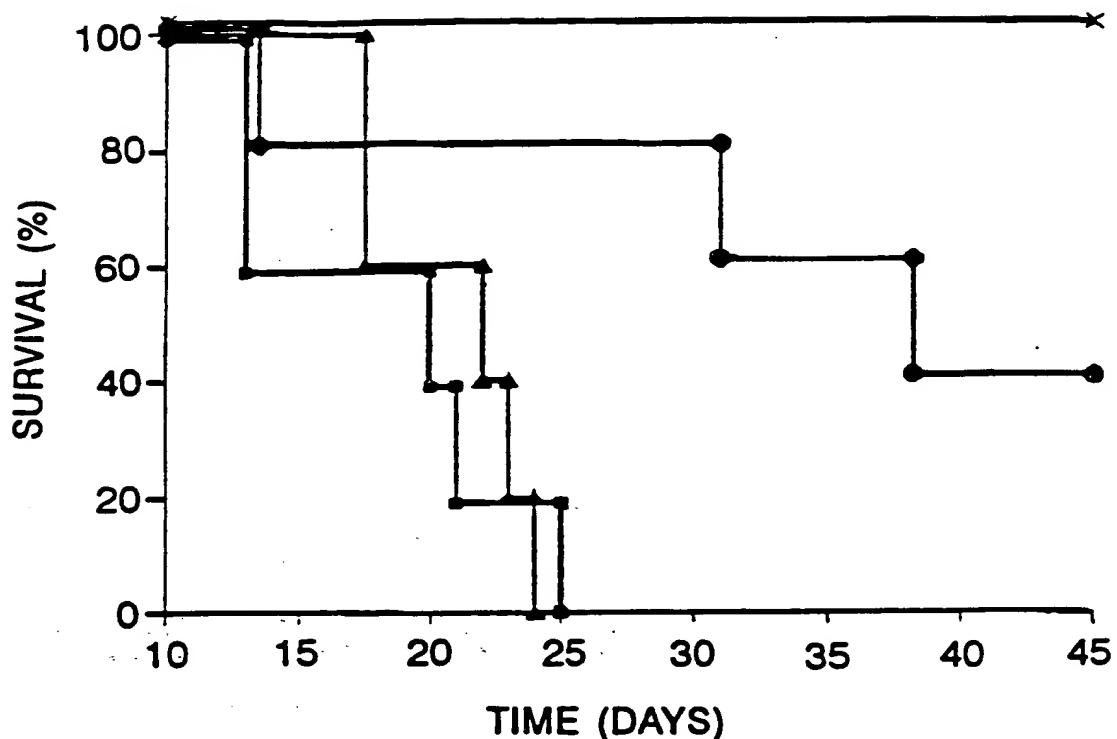
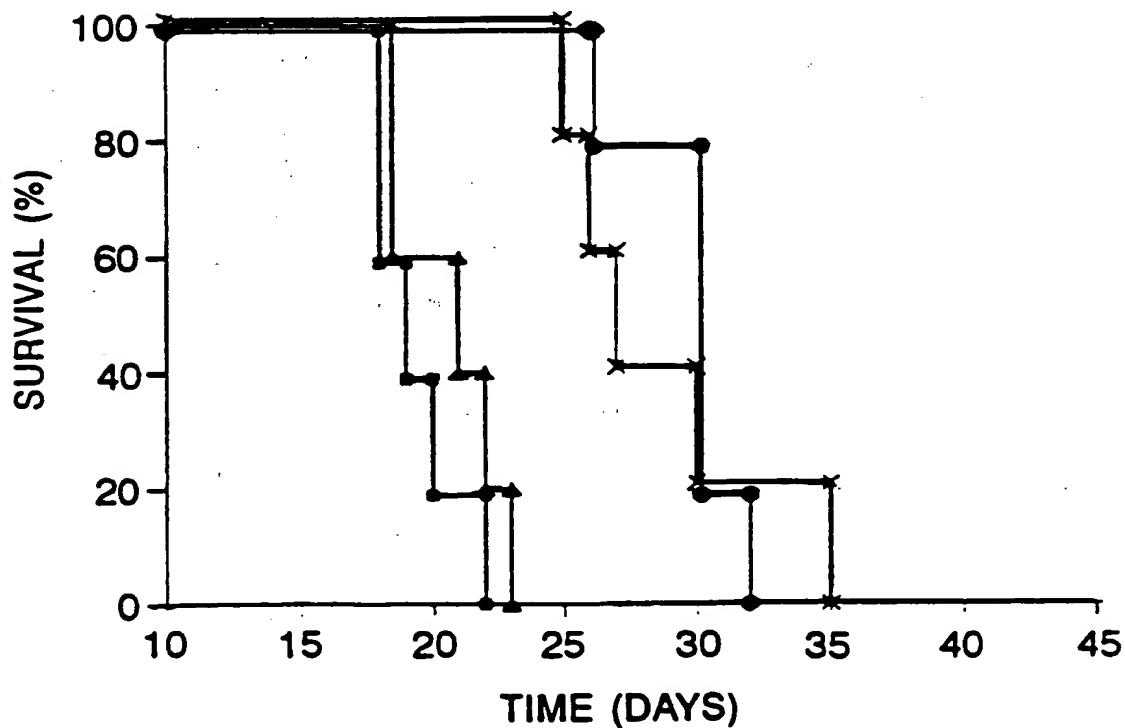
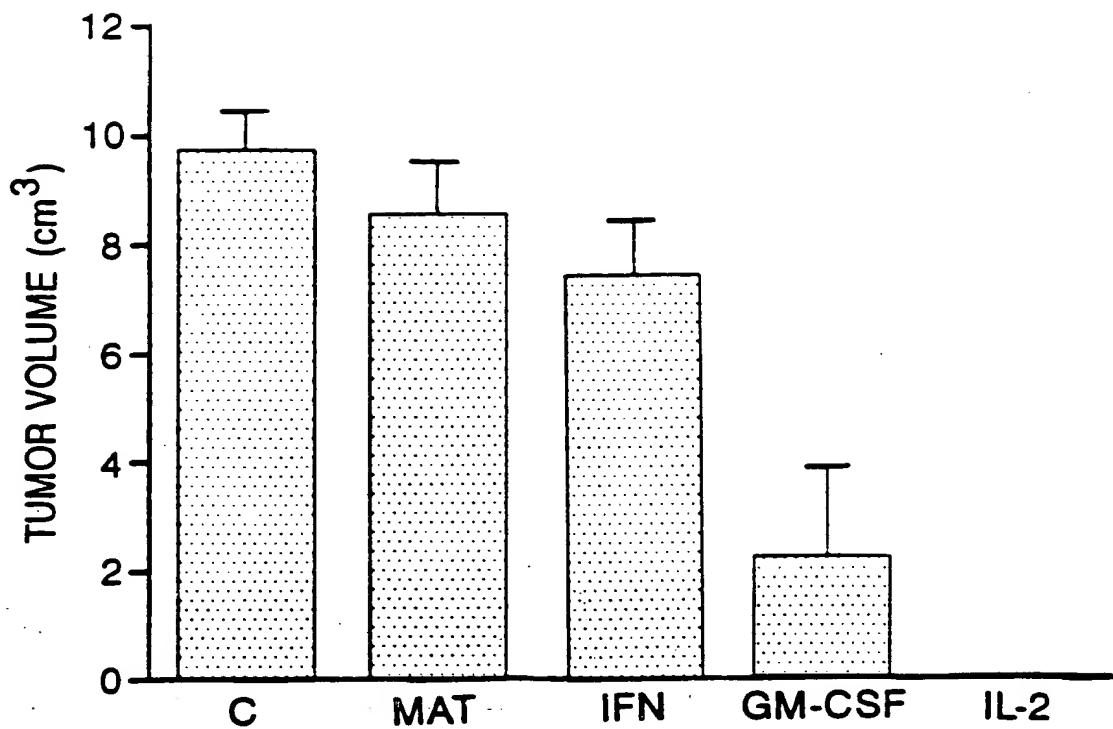
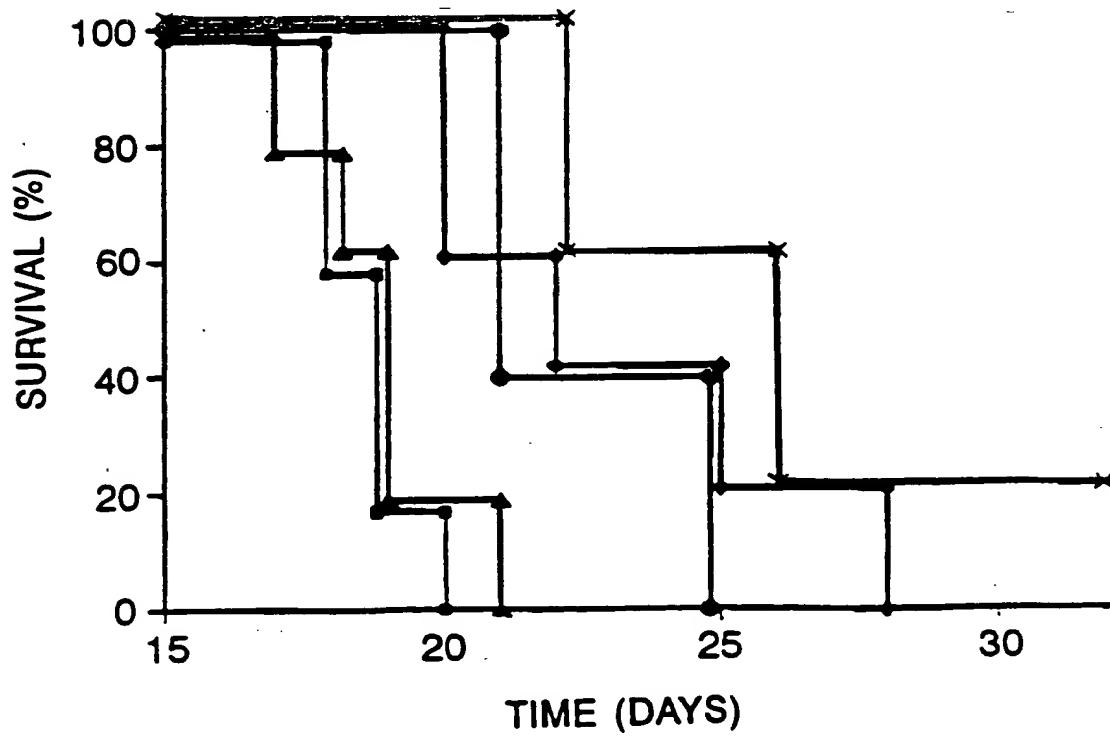


FIGURE 24B



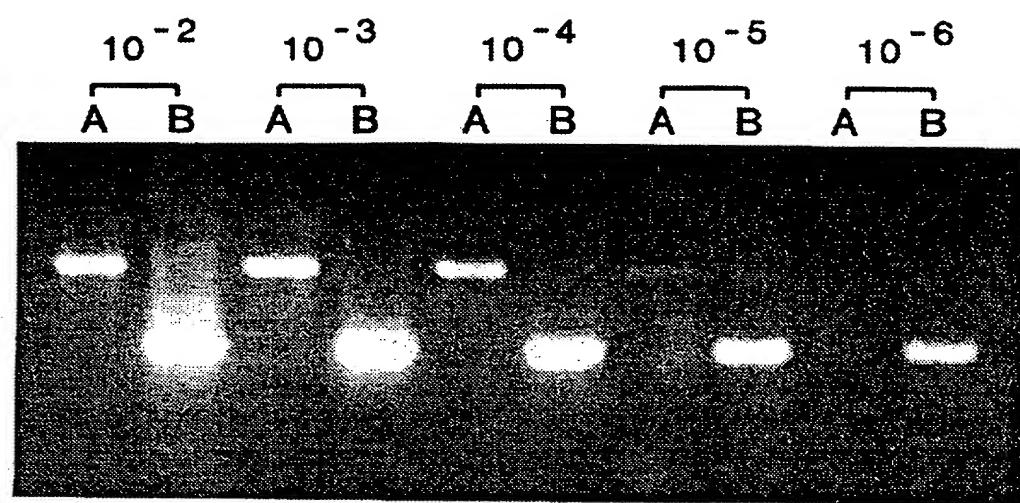
SUBSTITUTE SHEET (RULE 26)

FIGURE 25A**FIGURE 25B**

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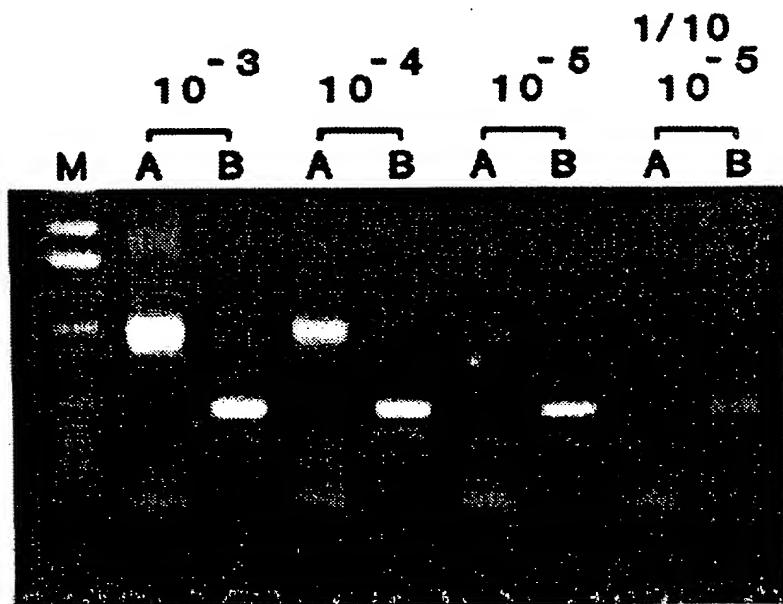
FIGURE 26



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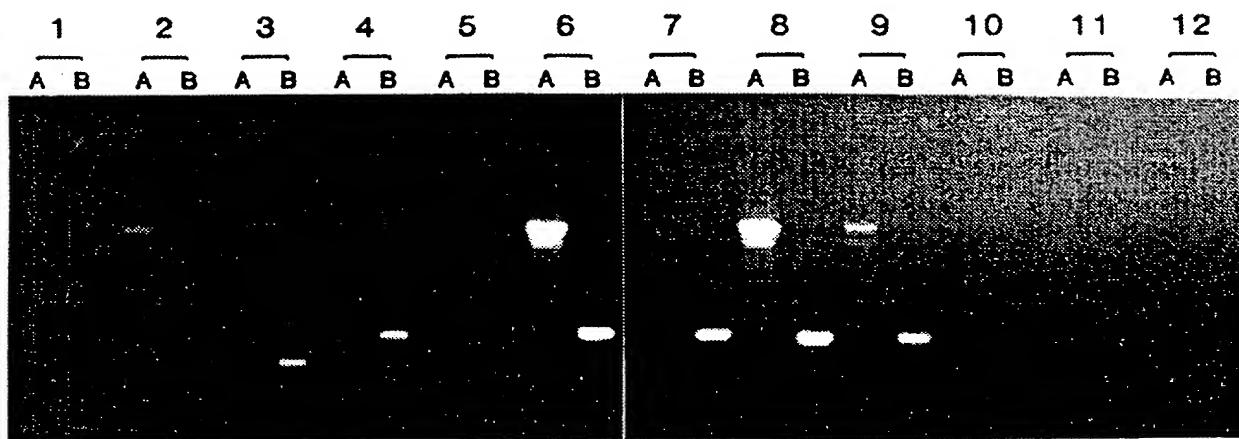
FIGURE 27



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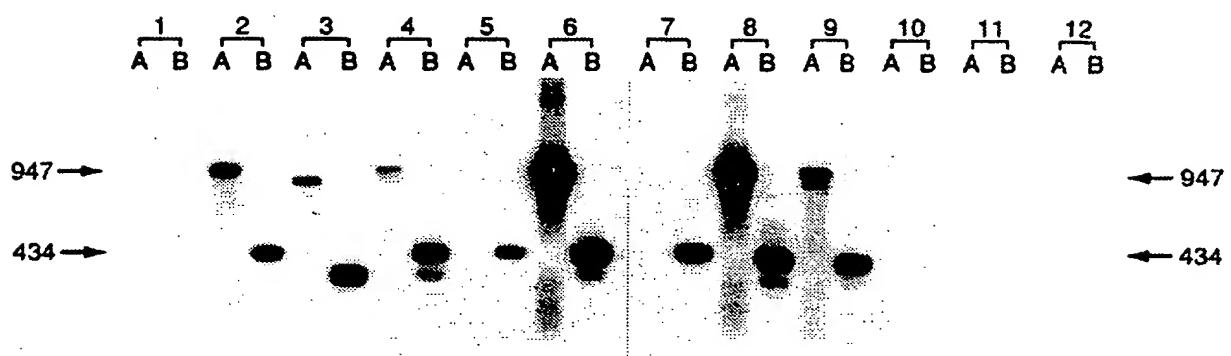
FIGURE 28



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FIGURE 29



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FIGURE 30

Patient	Stage	Treatment	PSA	PAP	PSA-PCR	PSM-PCR
1	T2NxMo	None	8.9	0.7	-	+
2	T2NoMo	RRP 7/93	6.1	-	-	+
3	T2CNoMo	PLND 5/93	4.5	0.1	-	+
4	T2BNoMo	RRP 3/92	NMA	0.4	-	+
5	T3NxMo	Proscar + Flutamide	51.3	1.0	-	+
6	Recur T3	I-125 1986	54.7	1.4	-	+
7	T3ANoMo	RRP 10/92	NMA	0.3	-	+
8	T3NxMo	XRT 1987	7.5	0.1	-	-
9	T3NxMo	Proscar + Flutamide	35.4	0.7	-	-
10	D2	S/P XRT Flutamide +Emcyt	311	4.5	+	+
11	D2	RRP 4/91 Lupron 10/92 Velban + Emcyt 12/92	1534	1.4	+	+
12	T2NoMo	RRP 8/91	NMA	0.5	-	+
13	T3NoMo	RRP 1/88 Lupron + Flutamide 5/92	0.1	0.3	-	-
14	D1	PLND 1989 XRT 1989	1.6	0.4	-	-
15	D1	Proscar + Flutamide	20.8	0.5	-	-
16	T2CNoMo	RRP 4/92	0.1	0.3	-	-